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APPLICATION NO.	FILING DATE	FIRST NAMED INVENTOR	ATTORNEY DOCKET NO.	CONFIRMATION NO.
09/874,991	06/07/2001	James J. Mond	07787.0042	5537
22852	7590	09/08/2004	EXAMINER	
FINNEGAN, HENDERSON, FARABOW, GARRETT & DUNNER LLP 1300 I STREET, NW WASHINGTON, DC 20005			MINNIFIELD, NITA M	
			ART UNIT	PAPER NUMBER
			1645	

DATE MAILED: 09/08/2004

Please find below and/or attached an Office communication concerning this application or proceeding.

Office Action Summary

Application No.

09/874,991

Applicant(s)

MOND ET AL.

Examiner

N. M. Minnifield

Art Unit

1645

-- The MAILING DATE of this communication appears on the cover sheet with the correspondence address --

Period for Reply

A SHORTENED STATUTORY PERIOD FOR REPLY IS SET TO EXPIRE 3 MONTH(S) FROM THE MAILING DATE OF THIS COMMUNICATION.

- Extensions of time may be available under the provisions of 37 CFR 1.136(a). In no event, however, may a reply be timely filed after SIX (6) MONTHS from the mailing date of this communication.
- If the period for reply specified above is less than thirty (30) days, a reply within the statutory minimum of thirty (30) days will be considered timely.
- If NO period for reply is specified above, the maximum statutory period will apply and will expire SIX (6) MONTHS from the mailing date of this communication.
- Failure to reply within the set or extended period for reply will, by statute, cause the application to become ABANDONED (35 U.S.C. § 133). Any reply received by the Office later than three months after the mailing date of this communication, even if timely filed, may reduce any earned patent term adjustment. See 37 CFR 1.704(b).

Status

- 1) ☒ Responsive to communication(s) filed on 10 June 2004.
- 2a) ☐ This action is **FINAL**. 2b) ☒ This action is non-final.
- 3) ☐ Since this application is in condition for allowance except for formal matters, prosecution as to the merits is closed in accordance with the practice under *Ex parte Quayle*, 1935 C.D. 11, 453 O.G. 213.

Disposition of Claims

- 4) ☒ Claim(s) 1-17 is/are pending in the application.
- 4a) Of the above claim(s) 11-17 is/are withdrawn from consideration.
- 5) ☐ Claim(s) _____ is/are allowed.
- 6) ☒ Claim(s) 1-10 is/are rejected.
- 7) ☐ Claim(s) _____ is/are objected to.
- 8) ☒ Claim(s) 11-17 are subject to restriction and/or election requirement.

Application Papers

- 9) ☒ The specification is objected to by the Examiner.
- 10) ☐ The drawing(s) filed on _____ is/are: a) ☐ accepted or b) ☐ objected to by the Examiner.
Applicant may not request that any objection to the drawing(s) be held in abeyance. See 37 CFR 1.85(a).
Replacement drawing sheet(s) including the correction is required if the drawing(s) is objected to. See 37 CFR 1.121(d).
- 11) ☐ The oath or declaration is objected to by the Examiner. Note the attached Office Action or form PTO-152.

Priority under 35 U.S.C. § 119

- 12) ☐ Acknowledgment is made of a claim for foreign priority under 35 U.S.C. § 119(a)-(d) or (f).
- a) ☐ All b) ☐ Some * c) ☐ None of:
- ☐ Certified copies of the priority documents have been received.
 - ☐ Certified copies of the priority documents have been received in Application No. _____.
 - ☐ Copies of the certified copies of the priority documents have been received in this National Stage application from the International Bureau (PCT Rule 17.2(a)).

* See the attached detailed Office action for a list of the certified copies not received.

Attachment(s)

- 1) ☒ Notice of References Cited (PTO-892) 2 sheets
- 2) ☐ Notice of Draftsperson's Patent Drawing Review (PTO-948)
- 3) ☒ Information Disclosure Statement(s) (PTO-1449 or PTO/SB/08)
Paper No(s)/Mail Date 10 sheets. 10/01/01; 9/7/01; 3/11/02
- 4) ☐ Interview Summary (PTO-413)
Paper No(s)/Mail Date. _____
- 5) ☐ Notice of Informal Patent Application (PTO-152)
- 6) ☐ Other: _____

DETAILED ACTION

1. Applicant's election with traverse of Group I, claims 1-10 and species SEQ ID NO: 2, 5, 6, 7, 12-17, in the reply filed on June 10, 2004 is acknowledged. The traversal is on the ground(s) that for a restriction requirement to be proper, the Examiner must show (1) that the inventions defined by the restricted groups of claims are independent and distinct, and (2) that there would be a serious burden on the Examiner if restriction was not required. M.P.E.P. 803. Applicants assert that the Examiner has focused on only the first part of this two-part test. In order to properly restrict the groups, the Examiner needs to show that there would be a serious burden in examining the claims together. Applicants submit that no such serious burden exists, and respectfully submit that withdrawal of the restriction requirement as to the claims of Groups I, II and V is appropriate. Specifically, because the claims of each group are directed to compositions comprising at least one oligonucleotide comprising both an RNA region and a DNA region, wherein at least one terminus of the oligonucleotide comprises RNA, this subject matter must be searched for each group. Thus, a thorough search and examination of Groups I, II, and V together does not represent an undue burden and Applicants respectfully request that the Examiner reconsider this restriction requirement. See M.P.E.P. 803 ("If the search and examination of the entire application can be made without serious burden, the examiner must examine it on the merits, even though it includes claims to independent or distinct inventions." (emphasis added)). Applicants expressly reserve their right, under M.P.E.P. 821.04, to add method claims to this application that depend from, or otherwise incorporate all limitations

of, the product claims of Groups I, II, and V for rejoinder with allowed product claims in this application.

This is not found persuasive. With regard to Applicants' assertions that there is no serious search burden to the Examiner to examine Groups I, II and V together, it is noted that a serious search burden is created because the Groups II and V would require additional search for the composition that comprises not only the RNA and DNA as set forth in the invention of Group I, but also the other ingredients claimed in Groups II and V, for example the antigen. The restriction Groups have acquired a separate status in the art as a separate subject for inventive effect and require independent searches. The search for each of the above inventions is not co-extensive particularly with regard to the literature search. A reference, which would anticipate the invention of one group would not necessarily anticipate or make obvious any of the other groups. Moreover, as to the question of burden of search, classification of subject matter is merely one indication of the burdensome nature of the search involved. The literature search, particularly relevant in this art, is not co-extensive and is much more important in evaluating the burden of search. Burden in examining materially different groups having materially different issues also exist. The restriction requirement between Groups I, II and V is maintained.

It is also noted that Applicants expressly reserve their right, under M.P.E.P. 821.04, to add method claims to this application that depend from, or otherwise incorporate all limitations of, the product claims of Group I for rejoinder with allowed product claims in this application. **Process claims that depend from or otherwise include all the limitations of the patentable product** will be entered as a matter of right if the amendment is presented prior to final rejection or allowance, whichever is earlier. Amendments, submitted after final rejection, are

governed by 37 CFR 1.116; amendments submitted after allowance are governed by 37 CFR 1.312.

In the event of rejoinder, the requirement for restriction between the product claims and the rejoined process claims will be withdrawn, and the rejoined process claims will be fully examined for patentability in accordance with 37 CFR 1.104. Thus, to be allowable, the rejoined claims must meet all criteria for patentability including the requirements of 35 U.S.C. 101, 102, 103, and 112. Until an elected product claim is found allowable, an otherwise proper restriction requirement between product claims and process claims may be maintained. Withdrawn process claims that are not commensurate in scope with an allowed product claim will not be rejoined. See "Guidance on Treatment of Product and Process Claims in light of *In re Ochiai*, *In re Brouwer* and 35 U.S.C. § 103(b)," 1184 O.G. 86 (March 26, 1996). Additionally, in order to retain the right to rejoinder in accordance with the above policy, Applicant is advised that the process claims should be amended during prosecution either to maintain dependency on the product claims or to otherwise include the limitations of the product claims. **Failure to do so may result in a loss of the right to rejoinder.**

Further, note that the prohibition against double patenting rejections of 35 U.S.C. 121 does not apply where the restriction requirement is withdrawn by the examiner before the patent issues. See MPEP § 804.01.

The requirement is still deemed proper and is therefore made FINAL.

2. Claims 11-17 have been withdrawn from further consideration pursuant to 37 CFR 1.142(b), as being drawn to a nonelected inventions, there being no

allowable generic or linking claim. Applicant timely traversed the restriction (election) requirement in the reply filed on June 10, 2004.

3. It is noted that elected SEQ ID NO: 2, 5, 6, and 7 have an effective filing date of June 7, 2000. These sequences were first disclosed in the provisional application 60/209797, filed June 7, 2000. Elected SEQ ID NO: 12-17 have an effective filing date of June 7, 2001. These sequences were first disclosed in the non-provisional application 09/874991, filed June 7, 2001.

4. Claims 8-10 are rejected under 35 U.S.C. 112, first paragraph, because the specification, while being enabling for *in vitro* use of the immunostimulatory compositions, does not reasonably provide enablement for *in vivo* use of the immunostimulatory compositions. The specification does not enable any person skilled in the art to which it pertains, or with which it is most nearly connected, to use the invention commensurate in scope with these claims.

The claims are directed to an immunostimulatory composition comprising at least a first oligonucleotide and a second oligonucleotide, wherein both the first and second oligonucleotides each contain at least one RNA region and at least one DNA region, wherein at least one terminus of each oligonucleotide comprises RNA. Claims are also recite that each of the oligonucleotides of the immunostimulatory composition elicits a different immune stimulation profile. Claims are directed to an adjuvant comprising at least one oligonucleotide comprising both an RNA region and a DNA region, wherein at least one terminus of the oligonucleotide comprises RNA.

It is noted that the compositions contemplate both *in vitro* and *in vivo* use of these compositions.

The specification discloses *in vitro* methods (simulation of Th1 And Th2 type cytokine production, release of IL-6, release of IFN-gamma, B cell proliferation, stimulation of IgM secretion) using human peripheral lymphocytes and SEQ ID NO: 2, 5, 6, 7, HDR (hybrid DNA and RNA) and SEQ ID NO: 1 (only DNA, as a control) (see specification examples 2-7 on pages 34-47 and Tables 1-9). The specification teaches that the HDR does indeed stimulate different immune stimulation profiles, but only via *in vitro* means. Applicants speculate in the specification that, "it is expected that the HDRs of the invention, including mixtures of HDRs that elicit complementary patterns of activation, will provide correspondingly superior improvement to Th1 and Th2 responses in a patient as compared to DNA-based oligonucleotides." (p. 36). However, the specification does set forth any enablement for HDRs eliciting a different immune stimulation profile in an animal or patient or adjuvant activity in an animal or patient. Examples 8-10 (see pages 48-50 of the specification) set forth a prophetic protocol of how one of skill in the art would do these *in vivo* experiments, not that there were actually performed or that the immune stimulation was achieved in the same manner as for the *in vitro* experiments in Examples 2-7. Example 8 states, that "HDR injected mice will show increased levels of total IgM as opposed to the PBS injected controls." (p. 48). Example 9 only shows *in vivo* use of SEQ ID NO: 2. Example 10 states that the "HDR injected animals *will show* elevated levels of anti-BSA ...". (p. 50). The specification further asserts that the list of HDRs (see pages 51-64) are illustrative sequences have been selected in light of ODN sequences known in the art to possess immunostimulatory activity (innate, global,

cellular and/or humoral), and in light of the surprising observation reported herein that hybrid RNA-DNA ONDs (HDRs) possess robust immunostimulatory activity both *in vitro* and *in vivo*. Using the teachings of Examples 1-10, or other assays commonly used in the art, the skilled artisan will recognize that such HDRs, and all other HDR sequences within the scope of the invention can be assayed *in vitro* or *in vivo* for immunostimulatory activity (see p. 51). However, none of the sequences listed on pages 51-64 have been tested and they are not of the same structure as the tested SEQ ID NO: 2. SEQ ID NO: 2 is a RDR (meaning it has RNA at both termini and a DNA, CpG, center) while SEQ ID NO: 12-17 are DR (meaning only one terminus is RNA). It is not clear that a DR will function in the same manner as a RDR in either an *in vitro* or *in vivo* situation.

The state of the art is not clear with regard to the *in vivo* use of a hybrid RNA/DNA. Cong et al 2003 (BBRC, 2003, 310:1133-1139) teach that hybrid DNA/RNA provide similar *in vitro* results as set forth in the specification, but does not teach that this is yet possible *in vivo*. Cong et al indicate that these compounds *may* permit the development of therapeutic agents for use against cancer, asthma, allergy and infectious diseases and as adjuvant, but this has not yet been accomplished (pp.1137-1138). The art only teaches the *in vitro* methods of these hybrid compounds. In view of the lack of teaching and guidance in the specification and the unpredictability in the art with regard to *in vivo* use of these hybrids to elicit a different immune stimulation profile there would be undue experimentation necessary for a skilled artisan to practice the scope of the claimed invention.

5. The following is a quotation of the appropriate paragraphs of 35 U.S.C. 102 that form the basis for the rejections under this section made in this Office action:

A person shall be entitled to a patent unless –

(b) the invention was patented or described in a printed publication in this or a foreign country or in public use or on sale in this country, more than one year prior to the date of application for patent in the United States.

(e) the invention was described in (1) an application for patent, published under section 122(b), by another filed in the United States before the invention by the applicant for patent or (2) a patent granted on an application for patent by another filed in the United States before the invention by the applicant for patent, except that an international application filed under the treaty defined in section 351(a) shall have the effects for purposes of this subsection of an application filed in the United States only if the international application designated the United States and was published under Article 21(2) of such treaty in the English language.

6. Claims 1-10 are rejected under 35 U.S.C. 102(e) as being anticipated by Raz et al (6534062 6613751 or 6552006).

Raz et al, 6534062 for example, discloses a RNA/DNA hybrid and the DNA has a CpG motif (col. 7, l. 1-33; cols. 20-21). Raz et al discloses modifications of the phosphate backbone, which include a phosphorathioate modification (col. 7). The prior art anticipates the claimed invention.

With regard to claims 9, “that each of the oligonucleotides of the immunostimulatory composition elicits a different immune stimulation profile” and claim 10, “an adjuvant comprising at least one oligonucleotide comprising both an RNA region and a DNA region, wherein at least one terminus of the oligonucleotide comprises RNA”, it is noted that the prior art discloses the structural components of the claimed invention. The properties defined in claim 9 are believed to inherent. With regard to claim 10, the recitation of “adjuvant” is viewed as intended use. A recitation of the intended use of the claimed invention must result in a structural difference between the claimed invention and the prior

art in order to patentably distinguish the claimed invention from the prior art. If the prior art structure is capable of performing the intended use, then it meets the claim. In a claim drawn to a process of making, the intended use must result in a manipulative difference as compared to the prior art. See *In re Casey*, 152 USPQ 235 (CCPA 1967) and *In re Otto*, 136 USPQ 458, 459 (CCPA 1963).

Since the Office does not have the facilities for examining and comparing applicants' compositions with the compositions of the prior art, the burden is on applicant to show a novel or unobvious differences between the claimed product and the product of the prior art (i.e., that the compositions of the prior art does not possess the same material structural and functional characteristics of the claimed compositions) See *In re Best*, 562 F.2d 1252, 195 USPQ 430 (CCPA 1977) and *In re Fitzgerald et al.*, 205 USPQ 594.

7. Claims 1-10 are rejected under 35 U.S.C. 102(b) as being anticipated by Fosnaugh et al 1989 (Molecular and Cellular Biology, Nov. 1989, 9/11:5215-5218).

Fosnaugh et al disclose the elected SEQ ID NO: 7. It is noted that the claims are directed to an immunostimulatory composition comprising: at least one oligonucleotide comprising both an RNA region and a DNA region, wherein at least one terminus of the oligonucleotide comprises RNA. The prior art discloses the RNA at either or both termini and a DNA sequence that has a CpG motif as claimed.

With regard to claims 9, "that each of the oligonucleotides of the immunostimulatory composition elicits a different immune stimulation profile" and claim 10, "an adjuvant comprising at least one oligonucleotide comprising

both an RNA region and a DNA region, wherein at least one terminus of the oligonucleotide comprises RNA”, it is noted that the prior art discloses the structural components of the claimed invention. The properties defined in claim 9 are believed to inherent. With regard to claim 10, the recitation of “adjuvant” is viewed as intended use. A recitation of the intended use of the claimed invention must result in a structural difference between the claimed invention and the prior art in order to patentably distinguish the claimed invention from the prior art. If the prior art structure is capable of performing the intended use, then it meets the claim. In a claim drawn to a process of making, the intended use must result in a manipulative difference as compared to the prior art. See *In re Casey*, 152 USPQ 235 (CCPA 1967) and *In re Otto*, 136 USPQ 458, 459 (CCPA 1963).

Since the Office does not have the facilities for examining and comparing applicants' compositions with the compositions of the prior art, the burden is on applicant to show a novel or unobvious differences between the claimed product and the product of the prior art (i.e., that the compositions of the prior art does not possess the same material structural and functional characteristics of the claimed compositions) See *In re Best*, 562 F.2d 1252, 195 USPQ 430 (CCPA 1977) and *In re Fitzgerald et al.*, 205 USPQ 594.

8. Claims 1-10 are rejected under 35 U.S.C. 102(e) as being anticipated by Lees et al 6632923 or Dumas et al 6639063.

Lees et al discloses the elected species SEQ ID NO: 16 (see SEQ ID NO: 51 of the patent).

Dumas et al discloses the elected species SEQ ID NO: 7 (see SEQ ID NO: 11708 of the patent).

With regard to claims 9, “that each of the oligonucleotides of the immunostimulatory composition elicits a different immune stimulation profile” and claim 10, “an adjuvant comprising at least one oligonucleotide comprising both an RNA region and a DNA region, wherein at least one terminus of the oligonucleotide comprises RNA”, it is noted that the prior art discloses the structural components of the claimed invention. The properties defined in claim 9 are believed to be inherent. With regard to claim 10, the recitation of “adjuvant” is viewed as intended use. A recitation of the intended use of the claimed invention must result in a structural difference between the claimed invention and the prior art in order to patentably distinguish the claimed invention from the prior art. If the prior art structure is capable of performing the intended use, then it meets the claim. In a claim drawn to a process of making, the intended use must result in a manipulative difference as compared to the prior art. See *In re Casey*, 152 USPQ 235 (CCPA 1967) and *In re Otto*, 136 USPQ 458, 459 (CCPA 1963).

Since the Office does not have the facilities for examining and comparing applicants' compositions with the compositions of the prior art, the burden is on applicant to show a novel or unobvious difference between the claimed product and the product of the prior art (i.e., that the compositions of the prior art does not possess the same material structural and functional characteristics of the claimed compositions) See *In re Best*, 562 F.2d 1252, 195 USPQ 430 (CCPA 1977) and *In re Fitzgerald et al.*, 205 USPQ 594.

9. Claims 1-10 are rejected under 35 U.S.C. 102(b) as being anticipated by Accession No. AP000792 and AP000728 published in the Database 1999.

Accession No. AP000792 and AP000728 disclose elected species SEQ ID NO: 6 (see the attached sequence search printout).

With regard to claims 9, “that each of the oligonucleotides of the immunostimulatory composition elicits a different immune stimulation profile” and claim 10, “an adjuvant comprising at least one oligonucleotide comprising both an RNA region and a DNA region, wherein at least one terminus of the oligonucleotide comprises RNA”, it is noted that the prior art discloses the structural components of the claimed invention. The properties defined in claim 9 are believed to be inherent. With regard to claim 10, the recitation of “adjuvant” is viewed as intended use. A recitation of the intended use of the claimed invention must result in a structural difference between the claimed invention and the prior art in order to patentably distinguish the claimed invention from the prior art. If the prior art structure is capable of performing the intended use, then it meets the claim. In a claim drawn to a process of making, the intended use must result in a manipulative difference as compared to the prior art. See *In re Casey*, 152 USPQ 235 (CCPA 1967) and *In re Otto*, 136 USPQ 458, 459 (CCPA 1963).

Since the Office does not have the facilities for examining and comparing applicants' compositions with the compositions of the prior art, the burden is on applicant to show a novel or unobvious difference between the claimed product and the product of the prior art (i.e., that the compositions of the prior art does not possess the same material structural and functional characteristics of the claimed compositions) See *In re Best*, 562 F.2d 1252, 195 USPQ 430 (CCPA 1977) and *In re Fitzgerald et al.*, 205 USPQ 594.

10. Claims 1-10 are rejected under 35 U.S.C. 102(b) as being anticipated by Bonaldo et al Genome Research, 1996, 6/9:791-806.

Bonaldo et al discloses the elected species SEQ ID NO: 6 (see the attached sequence search printout).

With regard to claims 9, “that each of the oligonucleotides of the immunostimulatory composition elicits a different immune stimulation profile” and claim 10, “an adjuvant comprising at least one oligonucleotide comprising both an RNA region and a DNA region, wherein at least one terminus of the oligonucleotide comprises RNA”, it is noted that the prior art discloses the structural components of the claimed invention. The properties defined in claim 9 are believed to inherent. With regard to claim 10, the recitation of “adjuvant” is viewed as intended use. A recitation of the intended use of the claimed invention must result in a structural difference between the claimed invention and the prior art in order to patentably distinguish the claimed invention from the prior art. If the prior art structure is capable of performing the intended use, then it meets the claim. In a claim drawn to a process of making, the intended use must result in a manipulative difference as compared to the prior art. See *In re Casey*, 152 USPQ 235 (CCPA 1967) and *In re Otto*, 136 USPQ 458, 459 (CCPA 1963).

Since the Office does not have the facilities for examining and comparing applicants' compositions with the compositions of the prior art, the burden is on applicant to show a novel or unobvious differences between the claimed product and the product of the prior art (i.e., that the compositions of the prior art does not possess the same material structural and functional characteristics of the claimed compositions) See *In re Best*, 562 F.2d 1252, 195 USPQ 430 (CCPA 1977) and *In re Fitzgerald et al.*, 205 USPQ 594.

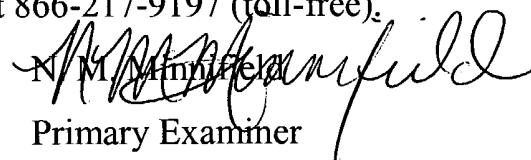
11. No claims are allowed.

12. The prior art made of record and not relied upon is considered pertinent to applicant's disclosure.

13. Any inquiry concerning this communication or earlier communications from the examiner should be directed to N. M. Minnifield whose telephone number is 571-272-0860. The examiner can normally be reached on M-F (8:00-5:30) Second Friday Off.

If attempts to reach the examiner by telephone are unsuccessful, the examiner's supervisor, Lynette R.F. Smith can be reached on 571-272-0864. The fax phone number for the organization where this application or proceeding is assigned is 703-872-9306.

Information regarding the status of an application may be obtained from the Patent Application Information Retrieval (PAIR) system. Status information for published applications may be obtained from either Private PAIR or Public PAIR. Status information for unpublished applications is available through Private PAIR only. For more information about the PAIR system, see <http://pair-direct.uspto.gov>. Should you have questions on access to the Private PAIR system, contact the Electronic Business Center (EBC) at 866-217-9197 (toll-free).


N. M. Minnifield
Primary Examiner
Art Unit 1645

NMM

August 31, 2004

FILE REFERENCE: GENSET.054PR2
CURRENT APPLICATION NUMBER: US/09/621.976
CURRENT FILING DATE: 2000-07-21
NUMBER OF SEQ ID NOS: 19335
SOFTWARE: Patent.pm
SEQ ID NO 12427
LENGTH: 129
TYPE: DNA
ORGANISM: Homo sapiens
US-09-621-976-12427

Query Match 97.3%; Score 29.2; DB 4; Length 129;
Best Local Similarity 93.3%; Pred. No. 13;
Matches 28; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAAAAAAAAAAGCGAAAAAAAAAAAAAAAA 30
Db 97 AAAAAAAAAAAGMSAAAAAAAAAAAAAAAA 126

RESULT 3

US-09-621-976-11708
Sequence 11708, Application US/09621976
Patent No. 6639063
GENERAL INFORMATION:
APPLICANT: Dumas Milne Edwards, J.B.
APPLICANT: Jobert, S.
TITLE OF INVENTION: ESTs and Encoded Human Proteins.
FILE REFERENCE: GENSET.054PR2
CURRENT APPLICATION NUMBER: US/09/621.976
CURRENT FILING DATE: 2000-07-21
NUMBER OF SEQ ID NOS: 19335
SOFTWARE: Patent.pm
SEQ ID NO 11708
LENGTH: 128
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc feature
LOCATION: 10.110
OTHER INFORMATION: n=a, g, c or t
US-09-621-976-11708

Query Match 96.7%; Score 29; DB 4; Length 128;
Best Local Similarity 96.7%; Pred. No. 14;
Matches 29; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 AAAAAAAAAAAGCGAAAAAAAAAAAAAAAA 30
Db 97 AAAAAAAAAAAGCGAAAAAAAAAAAAAAAA 126

RESULT 4

US-09-621-976-17033
Sequence 17033, Application US/09621976
Patent No. 6639063
GENERAL INFORMATION:
APPLICANT: Dumas Milne Edwards, J.B.
APPLICANT: Jobert, S.
TITLE OF INVENTION: ESTs and Encoded Human Proteins.
FILE REFERENCE: GENSET.054PR2
CURRENT APPLICATION NUMBER: US/09/621.976
CURRENT FILING DATE: 2000-07-21
NUMBER OF SEQ ID NOS: 19335
SOFTWARE: Patent.pm
SEQ ID NO 17033
LENGTH: 254
TYPE: DNA
ORGANISM: Homo sapiens
US-09-621-976-17033

Query Match 96.0%; Score 28.8; DB 4; Length 254;
Best Local Similarity 90.0%; Pred. No. 15;
Matches 27; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAAAAAAAAAAGCGAAAAAAAAAAAAAAAA 30
Db 222 AAAAAAAAAAAGSSAAAAAAAAAAAAAAAA 251

RESULT 5

US-09-621-976-14176
Sequence 14176, Application US/09621976
Patent No. 6639063
GENERAL INFORMATION:
APPLICANT: Dumas Milne Edwards, J.B.
APPLICANT: Jobert, S.
TITLE OF INVENTION: ESTs and Encoded Human Proteins.
FILE REFERENCE: GENSET.054PR2
CURRENT APPLICATION NUMBER: US/09/621.976
CURRENT FILING DATE: 2000-07-21
NUMBER OF SEQ ID NOS: 19335
SOFTWARE: Patent.pm
SEQ ID NO 14176
LENGTH: 77
TYPE: DNA
ORGANISM: Homo sapiens
US-09-621-976-14176

Query Match 94.7%; Score 28.4; DB 4; Length 77;
Best Local Similarity 96.7%; Pred. No. 20;
Matches 29; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 AAAAAAAAAAAGCGAAAAAAAAAAAAAAAA 30
Db 47 AAAAAAAAAAAGCGAAAAAAAAAAAAAAAA 76

RESULT 6

US-09-621-976-13606
Sequence 13606, Application US/09621976
Patent No. 6639063
GENERAL INFORMATION:
APPLICANT: Dumas Milne Edwards, J.B.
APPLICANT: Jobert, S.
TITLE OF INVENTION: ESTs and Encoded Human Proteins.
FILE REFERENCE: GENSET.054PR2
CURRENT APPLICATION NUMBER: US/09/621.976
CURRENT FILING DATE: 2000-07-21
NUMBER OF SEQ ID NOS: 19335
SOFTWARE: Patent.pm
SEQ ID NO 13606
LENGTH: 183
TYPE: DNA
ORGANISM: Homo sapiens
US-09-621-976-13606

Query Match 94.7%; Score 28.4; DB 4; Length 183;
Best Local Similarity 96.7%; Pred. No. 19;
Matches 29; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 AAAAAAAAAAAGCGAAAAAAAAAAAAAAAA 30
Db 132 AAAAAAAAAAAGCGAAAAAAAAAAAAAAAA 161

RESULT 7

US-09-621-976-10240
Sequence 10240, Application US/09621976
Patent No. 6639063
GENERAL INFORMATION:
APPLICANT: Dumas Milne Edwards, J.B.

FEATURES

Please mail of Action

141751 143058 contig of 1308 bp in length
143159 144610 contig of 1452 bp in length
144711 145763 contig of 1053 bp in length
145864 146911 contig of 1048 bp in length
147012 148183 contig of 1172 bp in length
148284 149304 contig of 1021 bp in length
149405 150594 contig of 1190 bp in length
Sequence updated (26-May-2000).
* NOTE: This is a 'working draft' sequence. It currently
* consists of 48 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.

7885: contig of 7885 bp in length
7886 13085: gap of 100 bp
7886 16310: contig of 8325 bp in length
16311 16410: gap of 100 bp
16411 22088: contig of 5678 bp in length
22089 22188: gap of 100 bp
22189 28358: contig of 6170 bp in length
28359 28458: gap of 100 bp
28459 34160: contig of 5702 bp in length
34161 34260: gap of 100 bp
34261 39101: contig of 4841 bp in length
39102 39201: gap of 100 bp
39202 44288: contig of 5087 bp in length
44289 44388: gap of 100 bp
44389 50127: contig of 5739 bp in length
50128 50227: gap of 100 bp
50228 55556: contig of 5329 bp in length
55557 55656: gap of 100 bp
55657 58778: contig of 3122 bp in length
58779 58878: gap of 100 bp
58879 62612: contig of 3734 bp in length
62613 62712: gap of 100 bp
62713 66184: contig of 3472 bp in length
66185 66284: gap of 100 bp
66285 70737: contig of 4453 bp in length
70738 70837: gap of 100 bp
70838 75172: contig of 4335 bp in length
75173 75272: gap of 100 bp
75273 79642: contig of 4370 bp in length
79643 79742: gap of 100 bp
79743 83579: contig of 3837 bp in length
83580 83679: gap of 100 bp
83680 86336: contig of 2657 bp in length
86337 86436: gap of 100 bp
86437 89885: contig of 3449 bp in length
89886 93305: contig of 3320 bp in length
93306 93405: gap of 100 bp
93406 96389: contig of 2984 bp in length
96390 96489: gap of 100 bp
96490 99699: contig of 3210 bp in length
99700 99799: gap of 100 bp
99800 102152: contig of 2353 bp in length
102153 102252: gap of 100 bp
102253 105419: contig of 3167 bp in length
105420 105519: gap of 100 bp
105520 108048: contig of 2529 bp in length
108049 108148: gap of 100 bp
108149 110751: contig of 2603 bp in length
110752 110851: gap of 100 bp
110852 114363: contig of 3512 bp in length
114364 114463: gap of 100 bp
114464 115521: contig of 1058 bp in length
115522 115621: gap of 100 bp
115622 117656: contig of 2035 bp in length
117657 117757: gap of 100 bp
117758 119830: contig of 2074 bp in length

119831 119930: gap of 100 bp
119931 122309: contig of 2379 bp in length
122310 122409: gap of 100 bp
122410 124103: contig of 1694 bp in length
124104 124203: gap of 100 bp
124204 126256: contig of 2053 bp in length
126257 126356: gap of 100 bp
126357 128377: contig of 2021 bp in length
128378 128477: gap of 100 bp
128479 130309: contig of 1832 bp in length
130310 130409: gap of 100 bp
130410 131990: contig of 1581 bp in length
131991 132090: gap of 100 bp
132091 133536: contig of 1446 bp in length
133537 133636: gap of 100 bp
133637 135395: contig of 1759 bp in length
135396 135495: gap of 100 bp
135496 137087: contig of 1592 bp in length
137088 137187: gap of 100 bp
137188 138305: contig of 1118 bp in length
138306 138405: gap of 100 bp
138406 139438: contig of 1033 bp in length
139439 139538: gap of 100 bp
139539 141650: contig of 2112 bp in length
141651 141750: gap of 100 bp
141751 143058: contig of 1308 bp in length
143059 143158: gap of 100 bp
143159 144610: contig of 1452 bp in length
144611 144710: gap of 100 bp
144711 145763: contig of 1053 bp in length
145764 145863: gap of 100 bp
145864 146911: contig of 1048 bp in length
146912 147011: gap of 100 bp
147012 148183: contig of 1172 bp in length
148184 148283: gap of 100 bp

Query Match 96.7%; Score 29; DB 2; Length 150594;
Best Local Similarity 100.0%; Pred. No. 13;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAAAAAAAAACCCGGGAAAAAAAAAAAA 29

Db 110717 AAAAAAAAAACCCGGGAAAAAAAAAAAA 110745

RESULT 4

ABI27405

LOCUS

DEFINITION

Accession

Version

Keywords

Source

Organism

Reference

Authors

Title

Journal

Reference

Authors

Title

Journal

Submitted

10-24, Tsuruga, Fukui 914-0047, Japan

(E-mail: axio.sugiyama@bio.toyobo.co.jp, Tel: 81-770-22-7643,

Fax: 80-770-22-7671)

Location/Qualifiers

1. 4127

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

ABI27405 Homo sapiens SNIP mRNA for SNAP-25-interacting protein, complete cds. 4127 bp mRNA linear PRI 04-DEC-2003

Accession

Version

Keywords

Source

Organism

Reference

Authors

Title

Journal

Submitted

10-24, Tsuruga, Fukui 914-0047, Japan

(E-mail: axio.sugiyama@bio.toyobo.co.jp, Tel: 81-770-22-7643,

Fax: 80-770-22-7671)

Location/Qualifiers

1. 4127

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

Sugiyama, A., Inoue, H. and Oka, M.

Homo sapiens cDNA, SNIP homolog

Published Only in Database (2003)

2 (bases 1 to 4127)

Sugiyama, A.

Direct Submission

Submitted (02-DEC-2003) Axio Sugiyama, TOYOBO CO., LTD; Toyocyo

10-24, Tsuruga, Fukui 914-0047, Japan

(E-mail: axio.sugiyama@bio.toyobo.co.jp, Tel: 81-770-22-7643,

Fax: 80-770-22-7671)

Location/Qualifiers

1. 4127

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

Please mail w/ Action

Fax: 81-75-705-1113
Ciona intestinalis cDNA Project (URL:
http://ghost.zool.kyoto-u.ac.jp/indexri.html).

FEATURES

source
1. 1458
/organism="Ciona intestinalis"
/mol_type="mRNA"
/db_xref="taxon:7719"
/clone="cieg056p11"

ORIGIN

Query Match 100.0%; Score 30; DB 3; Length 1458;
Best Local Similarity 100.0%; Pred. No. 3.6e+02;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 AAAAAAAAAACGAAAAAAAAAAAAA 30
DB 1425 AAAAAAAAAACGAAAAAAAAAAAAA 1454

RESULT 6

AY080787 1538 bp mRNA linear PLN 18-SEP-2002
LOCUS Arabidopsis thaliana putative enoyl-CoA hydratase (At4g31810) mRNA,
complete cds.

ACCESSION

AY080787 GI:19424018

VERSION

FLI CDNA.

KEYWORDS

Arabidopsis thaliana (thale cress)
Eukaryotes; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids I; Brassicales; Brassicaceae; Arabidopsis.

REFERENCE

1 (bases 1 to 1538)
Yamada, K., Liu, S.X., Sakano, H., Pham, P.K., Banh, J., Chung, M.K.,
Goldsmith, A.D., Lee, J.M., Quach, H.L., Toriumi, M., Yu, G., Bowser, L.,
Carninci, P., Chen, H., Cheuk, R., Hayashizaki, Y., Ishida, J.,
Jones, T., Kamiya, A., Karlin-Neumann, G., Kawai, J., Kim, C., Lam, B.,
Lin, J., Miranda, M., Narusaka, M., Nguyen, M., Palm, C.J., Sakurai, T.,
Satou, M., Seki, M., Shinn, P., Southwick, A., Shinozaki, K.,
Davis, R.W., Ecker, J.R., and Theologis, A.
Arabidopsis Full Length cDNA Clones
Unpublished

TITLE

Arabidopsis Full Length cDNA Clones

JOURNAL

2 (bases 1 to 1538)

REFERENCE

Yamada, K., Banh, J., Chan, M.M., Chang, C.H., Chang, E., Dale, J.M.,
Deng, J.M., Goldsmith, A.D., Lee, J.M., Onodera, C.S., Quach, H.L.,
Tang, C.C., Toriumi, M., Wu, H.C., Yamamura, Y., Yu, G., Bowser, L.,
Carninci, P., Chen, H., Cheuk, R., Hayashizaki, Y., Ishida, J.,
Jones, T., Kamiya, A., Karlin-Neumann, G., Kawai, J., Kim, C., Lam, B.,
Lin, J., Meyers, M.C., Miranda, M., Narusaka, M., Nguyen, M., Palm, C.J.,
Sakurai, T., Satou, M., Seki, M., Shinn, P., Southwick, A.,
Shinozaki, K., Davis, R.W., Ecker, J.R., and Theologis, A.
Direct Submission
Submitted (19-FEB-2002) Plant Gene Expression Center, 800 Buchanan
Street, Albany, CA 94710, USA
RIKEN Genomic Sciences Center (GSC) members carried out the
collection and clustering of RAPL cDNAs (RAPL cDNA: RIKEN
Arabidopsis Full-length cDNA): Seki, M., Narusaka, M., Ishida, J.,
Satou, M., Kamiya, A., Sakurai, T., Carninci, P., Kawai, J.,
Hayashizaki, Y. and Shinozaki, K.

TITLE

The Salk, Stanford, PGSC (SSP) Consortium members carried out the
sequencing and annotation of the RAPL cDNAs: Yamada, K., Banh, J.,
Chan, M.M., Chang, C.H., Chang, E., Dale, J.M., Deng, J.M.,
Goldsmith, A.D., Lee, J.M., Onodera, C.S., Quach, H.L., Tang, C.C.,
Toriumi, M., Wu, H.C., Yamamura, Y., Yu, G., Bowser, L., Chen, H.,
Cheuk, R., Jones, T., Karlin-Neumann, G., Kim, C., Lam, B., Lin, J.,
Meyers, M.C., Miranda, M., Nguyen, M., Palm, C.J., Shinn, P.,
Southwick, A., Davis, R.W., Ecker, J.R. and Theologis, A.

COMMENT

Yamada, K. (SSP/PGSC) and Seki, M. (RIKEN GSC) contributed equally to
this work. Shinozaki, K. (RIKEN GSC) and Theologis, A. (SSP/PGSC)
contributed equally to this work as PIs.

FEATURES

source
1. 1538
/organism="Arabidopsis thaliana"
/mol_type="mRNA"
/db_xref="taxon:3702"
/chromosomes="4"
/clone="RAFL05-21-G10 (R10305)"
/ecotype="Columbia"
/notes="This clone is in a modified pBluescript vector
(Lambda ZAP) as a XhoI/SstI insert."

gene

1. 1538
/genes="At4g31810"

5'UTR

1. 119
/genes="At4g31810"

CDS

20. 1249
/genes="At4g31810"
/codon_start=1
/evidence=experimental
/product="putative enoyl-CoA hydratase"
/protein_id="AA187270.1"
/db_xref="GI:19424019"

/translation="MGTVKALRVSEPLQWRSVSYGRRFALPNYSADADFDQVVL
VEGKASRAAILNPFSSNLNAPWGLKLYESWENPAISFVIMKSGKTCFSGA
DVLVLSHINSNGTESSKLFENLYFVLOQYTLKPNIAIMDVTMGCGGILSPGM
FRVATKTLVAHPVQIGFHPDAGASYLSRLPGYLGLALTGOKLNGVEMIAAGLA
TYVCLNARLPTEERIGKLLTDPDAVIDSLAQYGLVPPSSVSLHIELIDKYFGL
DVEETIEAMENEAANSNCNCKTKLKOIKASPLSLKITLQSIREGSPQTLDOCLTH
EYRISICGVSKVSGDFCEGIRARLVDPKAFKMPDPRLEDVSKDMVDCYTFPASELD
DSSELUKLPFAQREFIF"
1250. 1538
/genes="At4g31810"
1521. 1522
/genes="At4g31810"
/notes="artifact within poly A tail"

3'UTR

1250. 1538
/genes="At4g31810"

misc_feature

1521. 1522
/genes="At4g31810"

ORIGIN

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Best Local Similarity 100.0%; Pred. No. 3.6e+02;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY

1 AAAAAAAAAACGAAAAAAAAAAAAA 30

DB

1507 AAAAAAAAAACGAAAAAAAAAAAAA 1536

RESULT 7

DISP60A

LOCUS

DISP60A 1625 bp DNA linear INV 18-MAY-1994

DEFINITION

D.discoideum spore coat protein SP60 gene, complete cds.

ACCESSION

M26239

VERSION

M26239.1 GI:167885

KEYWORDS

major spore coat protein; spore protein.

SOURCE

Dictyostelium discoideum

ORGANISM

Dictyostelium discoideum

REFERENCE

Bukaryota; Mycetozoa; Dictyosteliida; Dictyostelium.

AUTHORS

Fosnaugh, K.L. and Loomis, W.F.

TITLE

Spore coat genes SP60 and SP70 of Dictyostelium discoideum

JOURNAL

Mol. Cell. Biol. 9 (11), 5215-5218 (1989)

MEDLINE

90097939

PubMed

2601718

REFERENCE

2 (bases 1 to 1625)

AUTHORS

Fosnaugh, K.L.

JOURNAL

Unpublished (1990)

COMMENT

Original source text: D.discoideum (strain Ax4), DNA (bp 1 to 693),
clones pSP[60,60.1], and cDNA to mRNA (bp 694 to 1560), clone
SP1.8
[2] revises [1].
Draft entry and computer readable sequence for [1] kindly submitted
by K.Fosnaugh, 13-JUL-1989.

FEATURES

source Location/Qualifiers
 1..1625
 /organism="Dictyostelium discoideum"
 /mol_type="genomic DNA"
 /db_xref="taxon:44689"
 <1..262
 /gene="SP60"
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 /note="precursor"
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 /product="spore coat protein"
 /protein_id="AA33251.1"
 /db_xref="GI:16786"
 translation="MKILSLVVGALCMGKVKYGEVNGDWNNGNNGWNNNGDWN
 NNGPILPCSTLQCPHYHCEVNGNRQVEDQITLPDFKCDNVHCPKGFNCYDWE
 KDALCVFWRPVPVTRCPGHECKVDWEGKCVKI KDDICDLRCPKGHECKIK
 HDGSKCVSWRPPRCPGHECKVDWEGKCVKI KDDICDLRCPKGHECKIK
 KGVYEKIKHDSKCCVKTPTKPCCKPNSCARDEKCVATKDRICVYKPTCDNTRCP
 NYHCICGKIDGKVPCKKARCDVFCPFHRCVERGKILCEFPFPPQPRSLDW
 AENENDRDYDDDDYDGDYDGDYDGDYDGDYDGDYDGDYDGDYDGDYDGDYD
 DWGNDWDDNDNDGDNWDDDFQDANDEWDY"
 109..177
 /gene="SP60"
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 /product="spore coat protein"
 263..383
 /gene="SP60"
 384..1560
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 /number=2

ORIGIN

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 Best Local Similarity 100.0%; Pred. No. 3.6e+02;
 Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAAAAAAAAAAGCGAAAAAAAAAAAAAAAA 30
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 DB 80 AAAAAAAAAAAGCGAAAAAAAAAAAAAAAA 109
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RESULT 8
 AB047834
 LOCUS Macaca fascicularis brain cDNA, clone:QcCE-16296. 1683 bp mRNA linear PRI 11-OCT-2001
 DEFINITION
 ACCESSION AB047834
 VERSION AB047834.1 GI:9967116
 KEYWORDS
 SOURCE Macaca fascicularis (crab-eating macaque)
 ORGANISM
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
 Cercopithecinae; Macaca.

REFERENCE
 1 Osada,N., Hida,M., Kusuda,J., Tanuma,R., Iseki,K., Hirata,M., Suto,Y., Hirai,M., Terao,K., Suzuki,Y., Sugano,S. and Hashimoto,K. Assignment of 118 novel cDNAs of cynomolgus monkey brain to human chromosomes
 Gene 275 (1), 31-37 (2001)
 JOURNAL 21458551
 MEDLINE 11574149
 PUBMED
 REFERENCE
 2 (bases 1 to 1683)
 Hashimoto,K., Osada,N., Hida,M., Kusuda,J. and Sugano,S.
 Direct Submission
 Submitted (28-AUG-2000) Katsuyuki Hashimoto, National Institute of Infectious Diseases, Division of Genetic Resources; 23-1, Toyama 1-chome, Shinjuku-ku, Tokyo 162-8640, Japan
 (E-mail:khashi@nih.go.jp, URL:http://www.nih.go.jp/yoken/genbank/)

COMMENT

Tel:81-3-5285-1111(ex.2120), Fax:81-3-5285-1181)
 Lab host: TOP10
 Vector: pME18S-FL3 (Acc.No. AB009864)
 R. Site1: DraIII (CACTGTTGG)
 R. Site2: DraIII (CACCATGTG)
 Description: 1st strand cDNA was primed with an oligo(dT) primer using specific 5' and 3' primers and amplified by PCR. The PCR product was digested with SfiI and size selection was performed to exclude fragments <1.5kb. The SfiI-digested PCR product was cloned into distinct DraIII sites of pME18S-FL3. XhoI sites just outside the DraIII sites can be used to isolate the cDNA insert. Libraries were constructed by Sugano et al. (University of Tokyo, Institute of Medical Science). Custom primer used for sequencing
 (5' end primer [CTTCGCTCTAAAGCTCG];
 3' end primer [CGACCTGCAGCTCGACCA]).

FEATURES

source Location/Qualifiers
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 /organism="Macaca fascicularis"
 /mol_type="mRNA"
 /db_xref="taxon:9541"
 /clone="QcCE-16296"
 /sex="male"
 /tissue type="cerebellum cortex"
 /clone lib="macaque brain cDNA library QcCE"
 /dev stage="adult"
 /lab_host="TOP10"
 14..1360
 /codon_start=1
 /product="hypothetical protein"
 /protein_id="BAB12260.1"
 /db_xref="GI:9967117"

CDS

translation="MSGMYRCOTSCVNGFNKPREALVOLIVQPPAVEPAELEIRG
 QDRVTMSCVLEAYPIRLVITYEWELGNKLLITGQFDSQSEYIEYFKVSLNENYGVN
 CSIINPAGRCSTLVIGKAYAPFYIDYINPQNRHRYISLQWNTQNDPAVDRI
 VAYRLGIRGAGQRMWEQIKNGINQKGLITNLTELKPEAEVRLTJTKFGE
 DSTIRIKYAPNPHLEPHCFHGFEDNCLFTQDDTDFDKSTARTNTKFTGT
 GPNADRSKGEFYMYIETSPRLGKLLSPVSIAPKNPYGTTNTAYCPSPYH
 MYGHCIGLVNYLRKQFTIENPSSSGNGKQWNEAHVNIYPTISQQLIFEGIRG
 PGIEGDIADIVSIAEGEAKQDLATKNSVDGAVGLVHFWLFPILVLSILSPRR"

ORIGIN

Query Match 100.0%; Score 30; DB 9; Length 1683;
 Best Local Similarity 100.0%; Pred. No. 3.6e+02;
 Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAAAAAAAAAAGCGAAAAAAAAAAAAAAAA 30
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 DB 1652 AAAAAAAAAAAGCGAAAAAAAAAAAAAAAA 1681
 |||||

RESULT 9

BT003906
 LOCUS Arabidopsis thaliana clone RAF15-13-B15 (R20655) unknown protein (atg72110) mRNA, complete cds.
 DEFINITION
 ACCESSION BT003906
 VERSION BT003906.1 GI:28393038
 KEYWORDS
 SOURCE FLI CDNA.

ORGANISM

Arabidopsis thaliana (thale cress)
 Arabidopsis thaliana
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsi.

REFERENCE

AUTHORS
 Yamada,K., Chan,M.M., Chang,C.H., Dale,J.M., Huan,V.W., Lee,J.M., Onodera,C.S., Quach,H.L., Tang,C., Toriumi,M., Wong,C., Wu,H.C., Yu,G., Yuan,S., Carninci,P., Chen,H., Cheuk,R., Hayashizaki,Y., Ishida,J., Jones,T., Kamiya,A., Kawai,J., Kim,C.J., Narusaka,M., Nguyen,M., Palm,C.J., Sakurai,T., Satou,M., Seki,M., Shinn,P., Southwick,A., Tripp,M.G., Wu,T., Shinozaki,K., Davis,R.W., Ecker,J.R. and Theologis,A.
 Arabidopsis Full Length cDNA Clones

PLEASE MAIL w ACTION

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: August 27, 2004, 05:18:34 ; Search time 1517.85 Seconds
(without alignments)
590.218 Million cell updates/sec

Title: US-09-874-991C-6
Perfect score: 30
Sequence: 1 aaaaaaaaaaacccgggaaaaaaaaa 30

Scoring table: IDENTITY_NUC
Gapop 10.0, Gapext 1.0

Searched: 27513289 seqs, 14931090276 residues

Total number of hits satisfying chosen parameters: 55026578

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

EST:*

1: em_estba:*

2: em_esthum:*

3: em_estin:*

4: em_estmu:*

5: em_estov:*

6: em_estov:*

7: em_estro:*

8: em_htc:*

9: gb_est1:*

10: gb_est2:*

11: gb_hc:*

12: gb_est3:*

13: gb_est4:*

14: gb_est5:*

15: em_estfun:*

16: em_estom:*

17: em_gss_hum:*

18: em_gss_inv:*

19: em_gss_pin:*

20: em_gss_vrt:*

21: em_gss_fun:*

22: em_gss_mam:*

23: em_gss_mus:*

24: em_gss_pro:*

25: em_gss_rtd:*

26: em_gss_phg:*

27: em_gss_vrl:*

28: gb_gss1:*

29: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	30	100.0	467	10	BE992043
2	30	100.0	887	13	BU944962
3	29.2	97.3	582	9	AL514409
4	29	96.7	244	14	CD215240

5	29	96.7	333	9	AI837622
6	29	96.7	427	14	CB476773
7	28.8	96.0	379	13	EX424970
8	28.8	96.0	855	13	EX393666
9	28.8	96.0	1201	13	EX393528
10	28.8	96.0	1201	13	EX445790
11	28.4	94.7	65	13	BQ389828
12	28.4	94.7	189	13	BQ389828
13	28.4	94.7	191	9	AI012754
14	28.4	94.7	214	9	AI012754
15	28.4	94.7	237	9	AI012754
16	28.4	94.7	263	14	CF337553
17	28.4	94.7	281	14	CA738092
18	28.4	94.7	326	10	BE104228
19	28.4	94.7	369	14	CB721366
20	28.4	94.7	391	9	AI541315
21	28.4	94.7	391	9	AV646715
22	28.4	94.7	400	14	CB077538
23	28.4	94.7	405	14	CF656383
24	28.4	94.7	414	13	BQ845683
25	28.4	94.7	421	29	CE230334
26	28.4	94.7	442	13	BQ521746
27	28.4	94.7	446	14	CF879286
28	28.4	94.7	473	14	CB077542
29	28.4	94.7	478	12	BM117544
30	28.4	94.7	508	13	BQ527846
31	28.4	94.7	513	29	AL952398
32	28.4	94.7	525	12	BI491724
33	28.4	94.7	557	13	BQ397970
34	28.4	94.7	644	14	CB34617
35	28.4	94.7	672	14	CB319854
36	28.4	94.7	696	29	CG789315
37	28.4	94.7	703	13	BU181322
38	28.4	94.7	723	9	AV710036
39	28.4	94.7	796	14	CD538077
40	28.4	94.7	856	28	AZ175573
41	28.4	94.7	877	13	BU531207
42	28.4	94.7	886	13	BQ441825
43	28.4	94.7	959	13	BX371183
44	28.4	94.7	1019	14	CF587086
45	28.4	94.7	1201	9	AL554915

ALIGNMENTS

RESULT 1

BE992043

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

MEDLINE

PubMed

COMMENT

BE992043 467 bp mRNA linear EST 05-OCT-2000
UI-M-BZ1-bec-d-04-0-UI-s1 NIH BMAP_MH12_s1 Mus musculus cDNA clone
UI-M-BZ1-bec-d-04-0-UI-3', mRNA sequence.

BE992043 1 GI:10672511

EST.

Mus musculus (house mouse)

Mus musculus

Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.

1 (bases 1 to 467)

Bonaldi, M.F., Leonon, G. and Soares, M.B.

Normalization and subtraction: two approaches to facilitate gene

discovery

Genome Res. 6 (9), 791-806 (1996)

97044477

8889548

Contact: Chin, H

National Institute of Mental Health

6001 Executive Blvd. Room 7N-7190, MSC 9643, Bethesda, MD

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Email: meste@mail.nih.gov

The sequence contained an oligo-dT track that was present in the

oligonucleotide that was used to prime the synthesis of first strand cDNA and therefore this may represent a bonafide poly A tail. The sequence tag present in the cDNA between the NotI site and the oligo-dr track served to verify it as a clone from the hippocampus tissue cDNA Library Preparation: M.B. Soares Lab Clone distribution: Researchers may obtain BMAP cDNA clones from RESEARCH GENETICS. It should be noted that Bento Soares is generating a small number of additional specialized non-redundant arrays of BMAP cDNAs whose availability will be considered under appropriate and limited collaborative arrangements the following repetitive elements were found in this cDNA sequence: 1-55, >POLY A#Simple_repeat 143-277, >POLY A#simple_repeat 361-432, >GC rich#low complexity

seq primer: M13 Forward
POLYA=yes.

FEATURES

source

Location/Qualifiers
1..467
/organism="Mus musculus"
/mol_type="mRNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clones="UI-M-B21-bec-d-04-0-UI"
/dev_stages="27-32 days"
/lab_host="DH10B (Life Technologies)"
/clone_lib="NIH BMAP_MHI2_S1"
/note="Vector: pVT3D-Pac (Pharmacia) with a modified polylinker; Site 1: Not I; Site 2: Eco RI; The NIH BMAP_MHI2_S1 library is a subtracted library derived from NIH BMAP_MHI2. NIH BMAP_MHI2 is a library derived from mouse hippocampus tissue. For a detailed description of the library from which this clone was derived, please visit our web site at brainest.eng.uiowa.edu.
TAG_TISSUE=hippocampus
TAG_LIB=NIH BMAP_MHI2_S1
TAG_SEQ=TAGTC"

ORIGIN

Query Match 100.0%; Score 30; DB 10; Length 467;
Best Local Similarity 100.0%; Pred. No. 6.1e+03;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAAAAAAAAAACCCGGGAAAAAAAAAAAA 30
|||||
DB 207 AAAAAAAAAAACCCGGGAAAAAAAAAAAA 236
|||||

RESULT 2
BU944962 887 bp mRNA linear EST 18-OCT-2002
LOCUS AGENCOURT 10546565 NIH MGC 141 Homo sapiens cDNA clone
DEFINITION IMAGE:673176 5', mRNA sequence.
BU944962
ACCESSION BU944962.1 GI:24133781
VERSION
KEYWORDS
SOURCE EST.
ORGANISM Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 887)
NIH-MGC http://mgi.nci.nih.gov/.

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: NCI
cDNA Library Preparation: Michael Brownstein Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM3062 row: f column: 23
High quality sequence stop: 303.

FEATURES

source

Location/Qualifiers
1..887
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:673176"
/tissue_type="mixed (pool of 40 RNAs)"
/lab_host="DH10B (T1 phage-resistant)"
/clone_lib="NIH_MGC_141"
/note="Vector: pDNR-LIB; Site 1: SfiI (ggcattatggcc); Site 2: SfiI (ggcgctctggcc); Double-stranded cDNA was prepared from a pool of 40 cell line polyA+ RNAs (bladder - 2%, blood - 33.4%, brain - 5.6%, breast - 12.5%, colon - 4%, connective tissue - 1.4%, eye - 1%, intestine - 2.6%, kidney - 2.2%, liver - 5.7%, lung - 10.8%, NK-cell - 5.2%, ovary - 4%, pharynx - 2.5%, prostate - 4.3%, salivary gland - 1.3%, and skin - 2.3%). 5' and 3' adaptors were used in cloning as follows:
5'-AAGCAGTGGTATCAACGAGTGGCCATTACGCGCGG-3' and
5'-ATTAGAGGCGGCGGCGGCGGACATG-dt(30)NN-3'. Full-length enriched library was constructed using the Clontech Creator SMART kit and size-selected to contain the 0.2-0.5 kb size fraction (other fractions present in NIH MGC 142). Library created in the laboratory of M. Brownstein (NIH). Note: this is a NIH_MGC Library."

Query Match 100.0%; Score 30; DB 13; Length 887;
Best Local Similarity 100.0%; Pred. No. 3.7e+03;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

ORIGIN

QY 1 AAAAAAAAAAACCCGGGAAAAAAAAAAAA 30
|||||
DB 341 AAAAAAAAAAACCCGGGAAAAAAAAAAAA 370
|||||

RESULT 3

AL514409

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

AL514409 582 bp mRNA linear EST 08-MAY-2003
AL514409 Homo sapiens NEUROBLASTOMA Homo sapiens cDNA clone
CLOBB009ZC11 3-PRIME, mRNA sequence.
AL514409 GI:30464294
EST.
Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 582)
Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
Full-length cDNA libraries and normalization
Unpublished (2001)
On Feb 13, 2001 this sequence version replaced gi:12777903.
Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: seqrefgenoscope.cns.fr; Web: www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 10492.f For
more information about this cluster, see
http://www.genoscope.cns.fr/
cgi-bin/cluster.cgi?seq=CLOBB009ZC11&cluster=10492.f. Contact:
Peng Liang Email: fliang@lifetech.com URL:
http://fulllength.invitrogen.com/ Invitrogen Corporation 1600
Paradise Avenue Genoscope sequence ID: CLOBB009ZC11FFI.

FEATURES

source

Location/Qualifiers
1..582
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CLOBB009ZC11"
/tissue_type="NEUROBLASTOMA"
/clone_lib="Homo sapiens NEUROBLASTOMA"

Please mail w/ Action

/notes="Vector: pCMVSPORT6; 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoRV sites of the pCMVSPORT 6 vector. Library was not normalized."

ORIGIN
Query Match 97.3%; Score 29.2; DB 9; Length 582;
Best Local Similarity 93.3%; Pred. No. 7.1e+03;
Matches 28; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
QY 1 AAAAAAAAAACCCGGGAAAAAAAAAAAA 30
Db 190 AAAAAAAAAACCCGGGAAAAAAAAAAAA 219

RESULT 4
CD215240 244 bp mRNA linear EST 20-MAY-2003
LOCUS
DEFINITION
Pgmn2n.pk014.f18 Normalized chicken muscle cDNA library (pgm2n)
Gallus gallus cDNA clone pgm2n.pk014.f18 5' similar to no
significant hits (pLog(P) > 4), mRNA sequence.

ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
CD215240.1 GI:30955051
EST.
Gallus gallus (chicken)
Gallus gallus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
Phasianinae; Gallus.

REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
1 (bases 1 to 244)
Cogburn, L.A. and Monson-O'Ornan, E.
Chicken ESTs from muscle
Unpublished (2002)
Contact: Larry A. Cogburn
University of Delaware
Townsend Hall, Newark, DE 19717, USA
Tel: 302-831-1335
Fax: 302-831-2822
Email: cogburn@udel.edu, www.chickest.udel.edu.

FEATURES
source
1..244
Location/Qualifiers
/organism="Gallus gallus"
/mol_type="mRNA"
/strain="Commercial broiler chickens, Ottawa Research Ctr
Strains 90 & 21"
/db_xref="taxon:9031"
/clone="pgm2n.pk014.f18"
/sex="Male and Female"
/issue_type="Brest muscle, leg muscle and epiphyseal
growth plate"
/dev_stage="Brest, leg; Embryo (d19); post-hatch (1d, 1.3, 5, 7, 9
11 weeks); growth plate (1d, 7d, 14d post-hatch)"
/lab_host="E. Coll. EMDH108"
/clone_lib="Normalized chicken muscle cDNA library
(pgm2n)"
/notes="Vector: pCMVSPORT6; Library made from equivalent
pools of total RNA isolated from each tissue (embryonic
muscle 33.3%; juvenile muscle 33.3%; and epiphyseal growth
plate 33.3% of the final RNA pool). Single pass sequencing
from 5'-end"

ORIGIN
Query Match 96.7%; Score 29; DB 14; Length 244;
Best Local Similarity 100.0%; Pred. No. 1.5e+04;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 AAAAAAAAAACCCGGGAAAAAAAAAAAA 29
Db 52 AAAAAAAAAACCCGGGAAAAAAAAAAAA 80

RESULT 5
CB476773 427 bp mRNA linear EST 26-MAR-2003
LOCUS

AI837622
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Mus musculus (house mouse)

REFERENCE
AUTHORS
TITLE
JOURNAL
MEDLINE
PUBMED
COMMENT
National Institute of Mental Health
6001 Executive Blvd. Room 7N-7190, MSC 9643, Bethesda, MD
20892-9643, USA
Tel: 301 443 1706
Fax: 301 443 9890
Email: MEST@mail.nih.gov
The sequence contained an oligo-dT track that was present in the
oligonucleotide that was used to prime the synthesis of first
strand cDNA and therefore this may represent a bonafide poly A
tail. The sequence tag present in the cDNA between the NotI site
and the oligo-dT track served to verify it as a clone from the
non-normalized hypothalamus library cDNA Library Preparation: M.B.
Soares Lab clone distribution: NIH BMAP cDNA clones will be made
available by the means that is soon to be determined. When NIH
determines the means for distribution of the BMAP cDNA clones, this
record will be updated accordingly when that means is determined.
Seq primer: M13 Forward
POLYA=Yes.

FEATURES
source
1..333
Location/Qualifiers
/organism="Mus musculus"
/mol_type="mRNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UI-M-AKO-adg-d-10-0-UI"
/dev_stage="27-32 days"
/lab_host="DHI08 (Life Technologies)"
/clone_lib="NIH BMAP_MHY"
/notes="Vector: PT7T3D-Pac (Pharmacia) with a modified
polylinker; Site 1: Not I; Site 2: Eco RI; The
NIH BMAP_MHY library is a non-normalized library
constructed from mouse hypothalamus. The tag is a string
of 5 nucleotides present between the Not I site and the
oligo-dT track. The library was constructed as described
by Bonaldo, Lennon and Soares, Genome Research 6:
791-806, 1996. Tissue provided by Ms. Annie Novakovich,
Zivic-Miller Laboratories.
TAG TISSUE=hypothalamus
TAG LIB=NIH BMAP_MHY
TAG_SEQ=CGGTa"

ORIGIN
Query Match 96.7%; Score 29; DB 9; Length 333;
Best Local Similarity 100.0%; Pred. No. 1.2e+04;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2 AAAAAAAAAACCCGGGAAAAAAAAAAAA 30
Db 262 AAAAAAAAAACCCGGGAAAAAAAAAAAA 290

RESULT 6
CB476773 427 bp mRNA linear EST 26-MAR-2003
LOCUS